

(1) GENERAL INFORMATION:

- 35
- 7,0370
- (i) APPLICANTS: Miyazono, Kohei; Dijke, Peter Ten; Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
- (ii) TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins Having Serine Threonine Kinase Domains And Their Use
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Felte & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/436,265
(B) FILING DATE: 30-October-1995
(C) CLASSIFICATION: 514
- B'
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/GB93/02367
(B) FILING DATE: 17-November-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9224057.1
(B) FILING DATE: 17-November-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9304677.9
(B) FILING DATE: 8-March-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9304680.3
(B) FILING DATE: 8-March-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9311047.6
(B) FILING DATE: 28-May-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9313763.6
(B) FILING DATE: 2-July-1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9136099.2
 (B) FILING DATE: 3-August-1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9321344.5
 (B) FILING DATE: 15-October-1993

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kohlei, Vineet
 (B) REGISTRATION NUMBER: 37,003
 (C) REFERENCE/DOCKET NUMBER: LUD 5298

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 688-9200
 (B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1984 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60
 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120
 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180
 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GTTCCGCCGA 240
 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC 294
 Met Thr Leu Gly
 1
 TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG 342
 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
 5 10 15 20

GGA	GAC	CCT	GTG	AAG	CCG	TCT	CGG	GGC	CCG	CTG	GTG	ACC	TGC	ACG	TGT	390
Gly	Asp	Pro	Val	Lys	Pro	Ser	Arg	Gly	Pro	Leu	Val	Thr	Cys	Thr	Cys	
				25					30					35		
GAG	AGC	CCA	CAT	TGC	AAG	GGG	CCT	ACC	TGC	CGG	GGG	GCC	TGG	TGC	ACA	438
Glu	Ser	Pro	His	Cys	Lys	Gly	Pro	Thr	Cys	Arg	Gly	Ala	Trp	Cys	Thr	
			40					45					50			
GTA	GTG	CTG	GTG	CGG	GAG	GAG	GGG	AGG	CAC	CCC	CAG	GAA	CAT	CGG	GGC	486
Val	Val	Leu	Val	Arg	Glu	Glu	Gly	Arg	His	Pro	Gln	Glu	His	Arg	Gly	
		55					60					65				
TGC	GGG	AAC	TTG	CAC	AGG	GAG	CTC	TGC	AGG	GGG	CGC	CCC	ACC	GAG	TTC	534
Cys	Gly	Asn	Leu	His	Arg	Glu	Leu	Cys	Arg	Gly	Arg	Pro	Thr	Glu	Phe	
	70					75					80					
GTC	AAC	CAC	TAC	TGC	TGC	GAC	AGC	CAC	CTC	TGC	AAC	CAC	AAC	GTG	TCC	582
Val	Asn	His	Tyr	Cys	Cys	Asp	Ser	His	Leu	Cys	Asn	His	Asn	Val	Ser	
	85				90					95					100	
CTG	GTG	CTG	GAG	GCC	ACC	CAA	CCT	CCT	TCG	GAG	CAG	CCG	GGA	ACA	GAT	630
Leu	Val	Leu	Glu	Ala	Thr	Gln	Pro	Pro	Ser	Glu	Gln	Pro	Gly	Thr	Asp	
				105					110					115		
GGC	CAG	CTG	GCC	CTG	ATC	CTG	GGC	CCC	GTG	CTG	GCC	TTG	CTG	GCC	CTG	678
Gly	Gln	Leu	Ala	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	Leu	Ala	Leu	
			120					125					130			
GTG	GCC	CTG	GGT	GTC	CTG	GGC	CTG	TGG	CAT	GTC	CGA	CGG	AGG	CAG	GAG	726
Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	Arg	Arg	Gln	Glu	
		135					140					145				
AAG	CAG	CGT	GGC	CTG	CAC	AGC	GAG	CTG	GGA	GAG	TCC	AGT	CTC	ATC	CTG	774
Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	Ser	Leu	Ile	Leu	
	150					155					160					
AAA	GCA	TCT	GAG	CAG	GGC	GAC	ACG	ATG	TTG	GGG	GAC	CTC	CTG	GAC	AGT	822
Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser	
	165				170					175					180	
GAC	TGC	ACC	ACA	GGG	AGT	GGC	TCA	GGG	CTC	CCC	TTC	CTG	GTG	CAG	AGG	870
Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	
				185					190					195		
ACA	GTG	GCA	CGG	CAG	GTT	GCC	TTG	GTG	GAG	TGT	GTG	GGA	AAA	GGC	CGC	918
Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys	Gly	Arg	
			200					205					210			
TAT	GGC	GAA	GTG	TGG	CGG	GGC	TTG	TGG	CAC	GGT	GAG	AGT	GTG	GCC	GTC	966
Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser	Val	Ala	Val	
		215					220					225				

AAG Lys 230	ATC Ile	TTC Phe	TCC Ser	TCG Ser	AGG Arg	GAT Asp 235	GAA Glu	CAG Gln	TCC Ser	TGG Trp	TTC Phe 240	CGG Arg	GAG Glu	ACT Thr	GAG Glu	1014
ATC Ile 245	TAT Tyr	AAC Asn	ACA Thr	GTA Val	TTG Leu 250	CTC Leu	AGA Arg	CAC His	GAC Asp	AAC Asn 255	ATC Ile	CTA Leu	GGC Gly	TTC Phe	ATC Ile 260	1062
GCC Ala	TCA Ser	GAC Asp	ATG Met	ACC Thr 265	TCC Ser	CGC Arg	AAC Asn	TCG Ser	AGC Ser 270	ACG Thr	CAG Gln	CTG Leu	TGG Trp	CTC Leu 275	ATC Ile	1110
ACG Thr	CAC His	TAC Tyr	CAC His 280	GAG Glu	CAC His	GGC Gly	TCC Ser	CTC Leu 285	TAC Tyr	GAC Asp	TTT Phe	CTG Leu	CAG Gln 290	AGA Arg	CAG Gln	1158
ACG Thr	CTG Leu	GAG Glu 295	CCC Pro	CAT His	CTG Leu	GCT Ala	CTG Leu 300	AGG Arg	CTA Leu	GCT Ala	GTG Val 305	TCC Ser	GCG Ala	GCA Ala	TGC Cys	1206
GGC Gly 310	CTG Leu	GCG Ala	CAC His	CTG Leu	CAC His	GTG Val 315	GAG Glu	ATC Ile	TTC Phe	GGT Gly 320	ACA Thr	CAG Gln	GGC Gly	AAA Lys	CCA Pro	1254
GCC Ala 325	ATT Ile	GCC Ala	CAC His	CGC Arg	GAC Asp 330	TTC Phe	AAG Lys	AGC Ser	CGC Arg	AAT Asn 335	GTG Val	CTG Leu	GTC Val	AAG Lys	AGC Ser 340	1302
AAC Asn	CTG Leu	CAG Gln	TGT Cys 345	TGC Cys	ATC Ile	GCC Ala	GAC Asp	CTG Leu	GGC Gly 350	CTG Leu	GCT Ala	GTG Val	ATG Met	CAC His 355	TCA Ser	1350
CAG Gln	GGC Gly	AGC Ser	GAT Asp 360	TAC Tyr	CTG Leu	GAC Asp	ATC Ile	GGC Gly 365	AAC Asn	AAC Asn	CCG Pro	AGA Arg	GTG Val 370	GGC Gly	ACC Thr	1398
AAG Lys	CGG Arg	TAC Tyr 375	ATG Met	GCA Ala	CCC Pro	GAG Glu	GTG Val 380	CTG Leu	GAC Asp	GAG Glu	CAG Gln	ATC Ile	CGC Arg	ACG Thr	GAC Asp	1446
TGC Cys 390	TTT Phe	GAG Glu	TCC Ser	TAC Tyr	AAG Lys	TGG Trp 395	ACT Thr	GAC Asp	ATC Ile	TGG Trp	GCC Ala 400	TTT Phe	GGC Gly	CTG Leu	GTG Val	1494
CTG Leu 405	TGG Trp	GAG Glu	ATT Ile	GCC Ala	CGC Arg 410	CGG Arg	ACC Thr	ATC Ile	GTG Val	AAT Asn 415	GGC Gly	ATC Ile	GTG Val	GAG Glu	GAC Asp 420	1542
TAT Tyr	AGA Arg	CCA Pro	CCC Pro	TTC Phe 425	TAT Tyr	GAT Asp	GTG Val	GTG Val	CCC Pro 430	AAT Asn	GAC Asp	CCC Pro	AGC Ser	TTT Phe 435	GAG Glu	1590

GAC	ATG	AAG	AAG	GTG	GTG	TGT	GTG	GAT	CAG	CAG	ACC	CCC	ACC	ATC	CCT	1638
Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	Pro	Thr	Ile	Pro	
			440					445					450			
AAC	CGG	CTG	GCT	GCA	GAC	CCG	GTC	CTC	TCA	GGC	CTA	GCT	CAG	ATG	ATG	1686
Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu	Ala	Gln	Met	Met	
		455					460					465				
CGG	GAG	TGC	TGG	TAC	CCA	AAC	CCC	TCT	GCC	CGA	CTC	ACC	GCG	CTG	CGG	1734
Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu	Thr	Ala	Leu	Arg	
	470					475					480					
ATC	AAG	AAG	ACA	CTA	CAA	AAA	ATT	AGC	AAC	AGT	CCA	GAG	AAG	CCT	AAA	1782
Ile	Lys	Lys	Thr	Leu	Gln	Lys	Ile	Ser	Asn	Ser	Pro	Glu	Lys	Pro	Lys	
485					490				495						500	
GTG	ATT	CAA	TAGCCCAGGA	GCACCTGATT	CCTTTCTGCC	TGCAGGGGGC										1831
Val	Ile	Gln														
TGGGGGGGGTG	GGGGGCAGTG	GATGGTGCCC	TATCTGGGTA	GAGGTAGTGT	GAGTGTGGTG											1891
TGTGCTGGGG	ATGGGCAGCT	GCGCCTGCCT	GCTCGGCCCC	CAGCCCACCC	AGCCAAAAAT											1951
ACAGCTGGGC	TGAAACCTGA	AAAAAAAAAA	AAA													1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
1 5 10 15

Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
20 25 30

Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
35 40 45

Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
50 55 60

Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
65 70 75 80

Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
85 90 95

His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
 100 105 110
 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
 115 120 125
 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
 130 135 140
 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
 145 150 155 160
 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
 165 170 175
 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
 180 185 190
 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
 195 200 205
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
 210 215 220
 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
 225 230 235 240
 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
 245 250 255
 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
 260 265 270
 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
 275 280 285
 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
 290 295 300
 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
 305 310 315 320
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
 325 330 335
 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
 340 345 350
 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
 355 360 365
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
 370 375 380

Ile	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala
385					390					395					400
Phe	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Val	Asn	Gly
				405					410					415	
Ile	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro	Asn	Asp
			420					425					430		
Pro	Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr
		435					440					445			
Pro	Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu
	450					455					460				
Ala	Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu
465					470					475					480
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Ile	Ser	Asn	Ser	Pro
				485					490					495	
Glu	Lys	Pro	Lys	Val	Ile	Gln									
				500											

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC	CCCAAGTGACC	AGAGTGAGAG	AAGCTCTGAA	CGAGGGCACG	CGGCTTGAAG											60
GACTGTGGGC	AGATGTGACC	AAGAGCCTGC	ATTAAGTTGT	ACA	ATG	GTA	GAT	GGA								115
							Met	Val	Asp	Gly						
							1									
GTG	ATG	ATT	CTT	CCT	GTG	CTT	ATC	ATG	ATT	GCT	CTC	CCC	TCC	CCT	AGT	163
Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu	Pro	Ser	Pro	Ser	
5					10					15					20	

ATG	GAA	GAT	GAG	AAG	CCC	AAG	GTC	AAC	CCC	AAA	CTC	TAC	ATG	TGT	GTG	211
Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu	Tyr	Met	Cys	Val	
				25					30					35		
TGT	GAA	GGT	CTC	TCC	TGC	GGT	AAT	GAG	GAC	CAC	TGT	GAA	GGC	CAG	CAG	259
Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys	Glu	Gly	Gln	Gln	
			40					45					50			
TGC	TTT	TCC	TCA	CTG	AGC	ATC	AAC	GAT	GGC	TTC	CAC	GTC	TAC	CAG	AAA	307
Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His	Val	Tyr	Gln	Lys	
		55					60					65				
GGC	TGC	TTC	CAG	GTT	TAT	GAG	CAG	GGA	AAG	ATG	ACC	TGT	AAG	ACC	CCG	355
Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr	Cys	Lys	Thr	Pro	
	70					75					80					
CCG	TCC	CCT	GGC	CAA	GCT	GTG	GAG	TGC	TGC	CAA	GGG	GAC	TGG	TGT	AAC	403
Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly	Asp	Trp	Cys	Asn	
85					90					95					100	
AGG	AAC	ATC	ACG	GCC	CAG	CTG	CCC	ACT	AAA	GGA	AAA	TCC	TTC	CCT	GGA	451
Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys	Ser	Phe	Pro	Gly	
				105					110					115		
ACA	CAG	AAT	TTC	CAC	TTG	GAG	GTT	GGC	CTC	ATT	ATT	CTC	TCT	GTA	GTG	499
Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile	Leu	Ser	Val	Val	
			120					125					130			
TTC	GCA	GTA	TGT	CTT	TTA	GCC	TGC	CTG	CTG	GGA	GTT	GCT	CTC	CGA	AAA	547
Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val	Ala	Leu	Arg	Lys	
		135					140					145				
TTT	AAA	AGG	CGC	AAC	CAA	GAA	CGC	CTC	AAT	CCC	CGA	GAC	GTG	GAG	TAT	595
Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg	Asp	Val	Glu	Tyr	
	150					155				160						
GGC	ACT	ATC	GAA	GGG	CTC	ATC	ACC	ACC	AAT	GTT	GGA	GAC	AGC	ACT	TTA	643
Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly	Asp	Ser	Thr	Leu	
165					170					175					180	
GCA	GAT	TTA	TTG	GAT	CAT	TCG	TGT	ACA	TCA	GGA	AGT	GGC	TCT	GGT	CTT	691
Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser	Gly	Ser	Gly	Leu	
				185					190					195		
CCT	TTT	CTG	GTA	CAA	AGA	ACA	GTG	GCT	CGC	CAG	ATT	ACA	CTG	TTG	GAG	739
Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile	Thr	Leu	Leu	Glu	
			200					205					210			
TGT	GTC	GGG	AAA	GGC	AGG	TAT	GGT	GAG	GTG	TGG	AGG	GGC	AGC	TGG	CAA	787
Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	Gln	
		215					220					225				

GGG Gly 230	GAA Glu	AAT Asn	GTT Val	GCC Ala	GTG Val	AAG Lys 235	ATC Ile	TTC Phe	TCC Ser	TCC Ser	CGT Arg 240	GAT Asp	GAG Glu	AAG Lys	TCA Ser	835
TGG Trp 245	TTC Phe	AGG Arg	GAA Glu	ACG Thr	GAA Glu 250	TTG Leu	TAC Tyr	AAC Asn	ACT Thr	GTG Val 255	ATG Met	CTG Leu	AGG Arg	CAT His	GAA Glu 260	883
AAT Asn	ATC Ile	TTA Leu	GGT Gly 265	TTC Phe	ATT Ile	GCT Ala	TCA Ser	GAC Asp 270	ATG Met	ACA Thr	TCA Ser	AGA Arg	CAC His	TCC Ser 275	AGT Ser	931
ACC Thr	CAG Gln	CTG Leu	TGG Trp 280	TTA Leu	ATT Ile	ACA Thr	CAT His	TAT Tyr 285	CAT His	GAA Glu	ATG Met	GGA Gly 290	TCG Ser	TTG Leu	TAC Tyr	979
GAC Asp	TAT Tyr	CTT Leu 295	CAG Gln	CTT Leu	ACT Thr	ACT Thr	CTG Leu 300	GAT Asp	ACA Thr	GTT Val	AGC Ser	TGC Cys 305	CTT Leu	CGA Arg	ATA Ile	1027
GTG Val 310	CTG Leu	TCC Ser	ATA Ile	GCT Ala	AGT Ser	GGT Gly 315	CTT Leu	GCA Ala	CAT His	TTG Leu	CAC His	ATA Ile	GAG Glu	ATA Ile	TTT Phe	1075
GGG Gly 325	ACC Thr	CAA Gln	GGG Gly	AAA Lys	CCA Pro 330	GCC Ala	ATT Ile	GCC Ala	CAT His	CGA Arg 335	GAT Asp	TTA Leu	AAG Lys	AGC Ser	AAA Lys 340	1123
AAT Asn	ATT Ile	CTG Leu	GTT Val	AAG Lys 345	AAG Lys	AAT Asn	GGA Gly	CAG Gln	TGT Cys 350	TGC Cys	ATA Ile	GCA Ala	GAT Asp	TTG Leu	GGC Gly 355	1171
CTG Leu	GCA Ala	GTC Val	ATG Met 360	CAT His	TCC Ser	CAG Gln	AGC Ser	ACC Thr 365	AAT Asn	CAG Gln	CTT Leu	GAT Asp	GTG Val 370	GGG Gly	AAC Asn	1219
AAT Asn	CCC Pro	CGT Arg 375	GTG Val	GGC Gly	ACC Thr	AAG Lys	CGC Arg 380	TAC Tyr	ATG Met	GCC Ala	CCC Pro	GAA Glu 385	GTT Val	CTA Leu	GAT Asp	1267
GAA Glu 390	ACC Thr	ATC Ile	CAG Gln	GTG Val	GAT Asp	TGT Cys 395	TTC Phe	GAT Asp	TCT Ser	TAT Tyr	AAA Lys 400	AGG Arg	GTC Val	GAT Asp	ATT Ile	1315
TGG Trp 405	GCC Ala	TTT Phe	GGA Gly	CTT Leu	GTT Val 410	TTG Leu	TGG Trp	GAA Glu	GTG Val 415	GCC Ala	AGG Arg	CGG Arg	ATG Met	GTG Val	AGC Ser 420	1363
AAT Asn	GGT Gly	ATA Ile	GTG Val	GAG Glu 425	GAT Asp	TAC Tyr	AAG Lys	CCA Pro	CCG Pro 430	TTC Phe	TAC Tyr	GAT Asp	GTG Val	GTT Val	CCC Pro 435	1411

AAT -GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA	1459
Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln	
440 445 450	
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC	1507
Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr	
455 460 465	
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA	1555
Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala	
470 475 480	
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT	1603
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn	
485 490 495 500	
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA	1650
Ser Leu Asp Lys Leu Lys Thr Asp Cys	
505	
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT	1710
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC	1770
GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA	1830
ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA	1890
<i>B' con.</i> AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG	1950
GCTTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT	2010
GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCTTTG	2070
CATTCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT	2130
GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA	2190
TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTTA CAATGATGCC GAACATTAGG	2250
AATTGTTTAT ACACAACTTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTTACAA	2310
AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA	2370
ATGTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT AAAATCACAT	2430
TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACTT TTTTTCAGTT CATATGCAGA	2490
ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA	2550
TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC AGAATTATCC	2610
ATTACGTGCA TTTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTTAAT CTACTTTTTG	2670

TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTTC AAGTCAAAAA AAAA

2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
 1 5 10 15
 Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
 20 25 30
 Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
 35 40 45
 Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
 50 55 60
 Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
 65 70 75 80
 Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
 85 90 95
 Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
 100 105 110
 Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
 115 120 125
 Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
 130 135 140
 Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
 145 150 155 160
 Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
 165 170 175
 Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
 180 185 190
 Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
 195 200 205
 Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
 210 215 220

Gly 225	Ser	Trp	Gln	Gly	Glu 230	Asn	Val	Ala	Val	Lys 235	Ile	Phe	Ser	Ser	Arg 240
Asp	Glu	Lys	Ser	Trp 245	Phe	Arg	Glu	Thr	Glu 250	Leu	Tyr	Asn	Thr	Val 255	Met
Leu	Arg	His	Glu 260	Asn	Ile	Leu	Gly	Phe 265	Ile	Ala	Ser	Asp	Met 270	Thr	Ser
Arg	His	Ser 275	Ser	Thr	Gln	Leu	Trp 280	Leu	Ile	Thr	His	Tyr 285	His	Glu	Met
Gly	Ser 290	Leu	Tyr	Asp	Tyr	Leu 295	Gln	Leu	Thr	Thr	Leu 300	Asp	Thr	Val	Ser
Cys 305	Leu	Arg	Ile	Val	Leu 310	Ser	Ile	Ala	Ser	Gly 315	Leu	Ala	His	Leu	His 320
Ile	Glu	Ile	Phe	Gly 325	Thr	Gln	Gly	Lys	Pro 330	Ala	Ile	Ala	His	Arg 335	Asp
Leu	Lys	Ser	Lys 340	Asn	Ile	Leu	Val	Lys 345	Lys	Asn	Gly	Gln	Cys 350	Cys	Ile
Ala	Asp	Leu 355	Gly	Leu	Ala	Val	Met 360	His	Ser	Gln	Ser	Thr 365	Asn	Gln	Leu
Asp 370	Val	Gly	Asn	Asn	Pro	Arg 375	Val	Gly	Thr	Lys	Arg 380	Tyr	Met	Ala	Pro
Glu 385	Val	Leu	Asp	Glu	Thr 390	Ile	Gln	Val	Asp	Cys 395	Phe	Asp	Ser	Tyr	Lys 400
Arg	Val	Asp	Ile	Trp 405	Ala	Phe	Gly	Leu	Val 410	Leu	Trp	Glu	Val	Ala 415	Arg
Arg	Met	Val	Ser 420	Asn	Gly	Ile	Val	Glu 425	Asp	Tyr	Lys	Pro	Pro 430	Phe	Tyr
Asp	Val	Val	Pro 435	Asn	Asp	Pro	Ser	Phe	Glu	Asp	Met	Arg 445	Lys	Val	Val
Cys 450	Val	Asp	Gln	Gln	Arg	Pro 455	Asn	Ile	Pro	Asn	Arg 460	Trp	Phe	Ser	Asp
Pro 465	Thr	Leu	Thr	Ser	Leu 470	Ala	Lys	Leu	Met	Lys 475	Glu	Cys	Trp	Tyr	Gln 480
Asn	Pro	Ser	Ala	Arg 485	Leu	Thr	Ala	Leu	Arg 490	Ile	Lys	Lys	Thr	Leu 495	Thr
Lys	Ile	Asp	Asn 500	Ser	Leu	Asp	Lys	Leu 505	Lys	Thr	Asp	Cys			

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2932 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 310..1905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT 60
 CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA 120
 AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG 180
 TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA 240
 TTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC 300
 AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348
 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala
 1 5 10
 TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396
 Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met
 15 20 25
 CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444
 Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu
 30 35 40 45
 AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC 492
 Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys
 50 55 60
 TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA 540
 Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile
 65 70 75
 ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA 588
 Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu
 80 85 90
 ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG 636
 Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln
 95 100 105

TGC	AAA	GAT	TCT	CCA	AAA	GCC	CAG	CTA	CGC	CGG	ACA	ATA	GAA	TGT	TGT	684
Cys	Lys	Asp	Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	
110					115					120					125	
CGG	ACC	AAT	TTA	TGT	AAC	CAG	TAT	TTG	CAA	CCC	ACA	CTG	CCC	CCT	GTT	732
Arg	Thr	Asn	Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	
				130					135					140		
GTC	ATA	GGT	CCG	TTT	TTT	GAT	GGC	AGC	ATT	CGA	TGG	CTG	GTT	TTG	CTC	780
Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	
			145					150					155			
ATT	TCT	ATG	GCT	GTC	TGC	ATA	ATT	GCT	ATG	ATC	ATC	TTC	TCC	AGC	TGC	828
Ile	Ser	Met	Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	
		160					165					170				
TTT	TGT	TAC	AAA	CAT	TAT	TGC	AAG	AGC	ATC	TCA	AGC	AGA	CGT	CGT	TAC	876
Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	
	175					180					185					
AAT	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	TTT	ATT	CCA	GTT	GGA	GAA	TCA	924
Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	
190					195					200					205	
CTA	AAA	GAC	CTT	ATT	GAC	CAG	TCA	CAA	AGT	TCT	GGT	AGT	GGG	TCT	GGA	972
Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	
				210					215					220		
CTA	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	GCC	AAA	CAG	ATT	CAG	ATG	GTC	1020
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	
			225					230					235			
CGG	CAA	GTT	GGT	AAA	GGC	CGA	TAT	GGA	GAA	GTA	TGG	ATG	GGC	AAA	TGG	1068
Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	
		240					245					250				
CGT	GGC	GAA	AAA	GTG	GCG	GTG	AAA	GTA	TTC	TTT	ACC	ACT	GAA	GAA	GCC	1116
Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	
	255					260					265					
AGC	TGG	TTT	CGA	GAA	ACA	GAA	ATC	TAC	CAA	ACT	GTG	CTA	ATG	CGC	CAT	1164
Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	
270					275					280					285	
GAA	AAC	ATA	CTT	GGT	TTC	ATA	GCG	GCA	GAC	ATT	AAA	GGT	ACA	GGT	TCC	1212
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	
				290					295					300		
TGG	ACT	CAG	CTC	TAT	TTG	ATT	ACT	GAT	TAC	CAT	GAA	AAT	GGA	TCT	CTC	1260
Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	
			305					310					315			

TAT Tyr	GAC Asp	TTC Phe 320	CTG Leu	AAA Lys	TGT Cys	GCT Ala 325	ACA Thr	CTG Leu	GAC Asp	ACC Thr	AGA Arg	GCC Ala 330	CTG Leu	CTT Leu	AAA Lys	1308
TTG Leu	GCT Ala 335	TAT Tyr	TCA Ser	GCT Ala	GCC Ala	TGT Cys 340	GGT Gly	CTG Leu	TGC Cys	CAC His	CTG Leu 345	CAC His	ACA Thr	GAA Glu	ATT Ile	1356
TAT Tyr 350	GGC Gly	ACC Thr	CAA Gln	GGA Gly	AAG Lys 355	CCC Pro	GCA Ala	ATT Ile	GCT Ala	CAT His 360	CGA Arg	GAC Asp	CTA Leu	AAG Lys	AGC Ser 365	1404
AAA Lys	AAC Asn	ATC Ile	CTC Leu	ATC Ile 370	AAG Lys	AAA Lys	AAT Asn	GGG Gly	AGT Ser 375	TGC Cys	TGC Cys	ATT Ile	GCT Ala	GAC Asp 380	CTG Leu	1452
GGC Gly	CTT Leu	GCT Ala	GTT Val 385	AAA Lys	TTC Phe	AAC Asn	AGT Ser 390	GAC Asp	ACA Thr	AAT Asn	GAA Glu	GTT Val 395	GAT Asp	GTG Val	CCC Pro	1500
TTG Leu	AAT Asn 400	ACC Thr	AGG Arg	GTG Val	GGC Gly	ACC Thr	AAA Lys 405	CGC Arg	TAC Tyr	ATG Met	GCT Ala 410	CCC Pro	GAA Glu	GTG Val	CTG Leu	1548
GAC Asp 415	GAA Glu	AGC Ser	CTG Leu	AAC Asn	AAA Lys	AAC Asn 420	CAC His	TTC Phe	CAG Gln	CCC Pro	TAC Tyr 425	ATC Ile	ATG Met	GCT Ala	GAC Asp	1596
ATC Ile 430	TAC Tyr	AGC Ser	TTC Phe	GGC Gly	CTA Leu 435	ATC Ile	ATT Ile	TGG Trp	GAG Glu	ATG Met 440	GCT Ala	CGT Arg	CGT Arg	TGT Cys	ATC Ile 445	1644
ACA Thr	GGA Gly	GGG Gly	ATC Ile 450	GTG Val	GAA Glu	GAA Glu	TAC Tyr	CAA Gln	TTG Leu 455	CCA Pro	TAT Tyr	TAC Tyr	AAC Asn	ATG Met 460	GTA Val	1692
CCG Pro	AGT Ser	GAT Asp	CCG Pro 465	TCA Ser	TAC Tyr	GAA Glu	GAT Asp	ATG Met 470	CGT Arg	GAG Glu	GTT Val	GTG Val	TGT Cys 475	GTC Val	AAA Lys	1740
CGT Arg	TTG Leu 480	CGG Arg	CCA Pro	ATT Ile	GTG Val	TCT Ser	AAT Asn 485	CGG Arg	TGG Trp	AAC Asn	AGT Ser	GAT Asp 490	GAA Glu	TGT Cys	CTA Leu	1788
CGA Arg 495	GCA Ala	GTT Val	TTG Leu	AAG Lys	CTA Leu	ATG Met 500	TCA Ser	GAA Glu	TGC Cys	TGG Trp	GCC Ala 505	CAC His	AAT Asn	CCA Pro	GCC Ala	1836
TCC Ser 510	AGA Arg	CTC Leu	ACA Thr	GCA Ala	TTG Leu 515	AGA Arg	ATT Ile	AAG Lys	AAG Lys	ACG Thr 520	CTT Leu	GCC Ala	AAG Lys	ATG Met	GTT Val 525	1884

GAA-TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT 1935
 Glu Ser Gln Asp Val Lys Ile
 530

AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT 1995
 AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTTACACAG GCTGCTAATA TTAAACCTTT 2055
 CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCAATTCTT TATATATGGA 2115
 CAGCTTTATT TTAAATGTGG TTTTIGATGC CTTTTTTTAA GTGGGTTTTT ATGAACTGCA 2175
 TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTC 2235
 ATAAAACGGT GCTTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA 2295
 AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTC TATTCTACCT TTGTAAAACA 2355
 GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC 2415
 TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTTGA 2475
 ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG 2535
 CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTACTTTGCA 2595
 AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA 2655
 AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTTCCTTC AACCACCATT TTTTTTGTGG 2715
 TTATTATTTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC 2775
 ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG 2835
 TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA 2895
 TATTTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC 2932

- (2) INFORMATION FOR SEQ ID NO: 6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 532 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe
 1 5 10 15
 Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
 20 25 30

Thr	Gly	Met	Lys	Ser	Asp	Ser	Asp	Gln	Lys	Lys	Ser	Glu	Asn	Gly	Val	
		35					40					45				
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	
	50					55					60					
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	
65					70					75					80	
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	
				85					90					95		
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	
			100					105					110			
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	
		115					120					125				
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	
	130					135					140					
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met	
145					150					155					160	
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	
				165					170					175		
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp	
			180					185					190			
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	
		195					200					205				
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	
	210					215					220					
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	
225					230					235					240	
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	
				245					250					255		
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	
			260					265					270			
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	
		275					280					285				
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	
	290					295					300					
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	
305					310					315					320	

Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
 325 330 335
 Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
 340 345 350
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
 355 360 365
 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
 370 375 380
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr
 385 390 395 400
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
 485 490 495
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
 500 505 510
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
 515 520 525
 Asp Val Lys Ile
 530

(2)- INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu	
1 5 10 15	
CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG	96
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu	
20 25 30	
CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA	144
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr	
35 40 45	
GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC	192
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His	
50 55 60	
CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG	240
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys	
65 70 75 80	
CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC	288
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys	
85 90 95	
TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC	336
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His	
100 105 110	
CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA	384
Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val	
115 120 125	
GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATC ATT	432
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile	
130 135 140	

54

GTT	TTC	CTT	GTC	ATT	AAC	TAT	CAT	CAG	CGT	GTC	TAT	CAC	AAC	CGC	CAG	480
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln	
145					150					155					160	
AGA	CTG	GAC	ATG	GAA	GAT	CCC	TCA	TGT	GAG	ATG	TGT	CTC	TCC	AAA	GAC	528
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp	
				165					170					175		
AAG	ACG	CTC	CAG	GAT	CTT	GTC	TAC	GAT	CTC	TCC	ACC	TCA	GGG	TCT	GGC	576
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly	
			180					185					190			
TCA	GGG	TTA	CCC	CTC	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	ACC	ATC	GTT	624
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val	
		195					200					205				
TTA	CAA	GAG	ATT	ATT	GGC	AAG	GGT	CGG	TTT	GGG	GAA	GTA	TGG	CGG	GGC	672
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	
	210					215					220					
CGC	TGG	AGG	GGT	GGT	GAT	GTG	GCT	GTG	AAA	ATA	TTC	TCT	TCT	CGT	GAA	720
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	
225					230					235					240	
GAA	CGG	TCT	TGG	TTC	AGG	GAA	GCA	GAG	ATA	TAC	CAG	ACG	GTC	ATG	CTG	768
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	
				245					250					255		
CGC	CAT	GAA	AAC	ATC	CTT	GGA	TTT	ATT	GCT	GCT	GAC	AAT	AAA	GAT	AAT	816
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	
			260					265					270			
GGC	ACC	TGG	ACA	CAG	CTG	TGG	CTT	GTT	TCT	GAC	TAT	CAT	GAG	CAC	GGG	864
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	
		275					280					285				
TCC	CTG	TTT	GAT	TAT	CTG	AAC	CGG	TAC	ACA	GTG	ACA	ATT	GAG	GGG	ATG	912
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met	
	290					295						300				
ATT	AAG	CTG	GCC	TTG	TCT	GCT	GCT	AGT	GGG	CTG	GCA	CAC	CTG	CAC	ATG	960
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	
305					310					315					320	
GAG	ATC	GTG	GGC	ACC	CAA	GGG	AAG	CCT	GGA	ATT	GCT	CAT	CGA	GAC	TTA	1008
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu	
				325					330					335		
AAG	TCA	AAG	AAC	ATT	CTG	GTG	AAG	AAA	AAT	GGC	ATG	TGT	GCC	ATA	GCA	1056
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala	
			340					345					350			

56

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GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCA	GTC	ACT	GAC	ACC	ATT	GAC	1104	
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp		
		355					360					365					
ATT	GCC	CCG	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	GCC	CCT	GAA	1152	
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu		
	370					375					380						
GTA	CTT	GAT	GAA	ACC	ATT	AAT	ATG	AAA	CAC	TTT	GAC	TCC	TTT	AAA	TGT	1200	
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys		
385					390					395					400		
GCT	GAT	ATT	TAT	GCC	CTC	GGG	CTT	GTA	TAT	TGG	GAG	ATT	GCT	CGA	AGA	1248	
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg		
				405				410						415			
TGC	AAT	TCT	GGA	GGA	GTC	CAT	GAA	GAA	TAT	CAG	CTG	CCA	TAT	TAC	GAC	1296	
Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp		
			420				425						430				
TTA	GTG	CCC	TCT	GAC	CCT	TCC	ATT	GAG	GAA	ATG	CGA	AAG	GTT	GTA	TGT	1344	
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys		
		435					440					445					
GAT	CAG	AAG	CTG	CGT	CCC	AAC	ATC	CCC	AAC	TGG	TGG	CAG	AGT	TAT	GAG	1392	
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu		
	450					455					460						
B' ant	GCA	CTG	CGG	GTG	ATG	GGG	AAG	ATG	ATG	CGA	GAG	TGT	TGG	TAT	GCC	AAC	1440
	Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	
	465					470					475					480	
GGC	GCA	GCC	CGC	CTG	ACG	GCC	CTG	CGC	ATC	AAG	AAG	ACC	CTC	TCC	CAG	1488	
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln		
				485				490						495			
CTC	AGC	GTG	CAG	GAA	GAC	GTG	AAG	ATC	TAACTGCTCC CTCTCTCCAC						1535		
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile									
			500					505									
ACGGAGCTCC	TGGCAGCGAG	AACTACGCAC				AGCTGCCGCG	TTGAGCGTAC	GATGGAGGCC							1595		
TACCTCTCGT	TTCTGCCCAG	CCCTCTGTGG				CCAGGAGCCC	TGGCCCGCAA	GAGGGACAGA							1655		
GCCCCGGGAGA	GA CTCGCTCA	CTCCCATGTT				GGGTTTGAGA	CAGACACCTT	TTCTATTTAC							1715		
CTCCTAATGG	CATGGAGACT	CTGAGAGCGA				ATTGTGTGGA	GA ACTCAGTG	CCACACCTCG							1775		
AACTGGTTGT	AGTGGAAGT	CCCGCGAAAC				CCGGTGCATC	TGGCACGTGG	CCAGGAGCCA							1835		
TGACAGGGGC	GCTTGGGAGG	GGCCGGAGGA				ACCGAGGTGT	TGCCAGTGCT	AAGCTGCCCT							1895		
GAGGGTTTCC	TTCGGGGACC	AGCCACAGC				ACACCAAGGT	GGCCCGGAAG	AACCAGAAGT							1955		

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GCAGCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTTCCCC TCCTCCCTGG GATGGACGCT 2015
 GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTTGT CTGTCCAGCC GTGTGTGCAT 2075
 GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCGTGCCAT GCCCTTACAC GTGCGTGTGA 2135
 GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG CATGTGCAGG 2195
 TCGGGGGTGT GGTCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTTCAG TAGTGAGCAG 2255
 CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCCAGAG CCCCTCATGC 2315
 CACAGTGGTA CTCTGTGT 2333

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
 1 5 10 15
 Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
 20 25 30
 Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
 35 40 45
 Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His
 50 55 60
 His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
 65 70 75 80
 Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
 85 90 95
 Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
 100 105 110
 Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val
 115 120 125
 Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
 130 135 140
 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
 145 150 155 160

59

Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp	
				165					170					175		
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly	
			180					185					190			
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val	
		195					200					205				
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	
	210					215					220					
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	
225					230					235					240	
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	
				245					250					255		
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	
			260					265					270			
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	
		275					280					285				
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met	
	290					295					300					
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	
305					310					315					320	
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu	
				325					330					335		
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala	
			340					345					350			
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp	
		355					360					365				
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	
	370					375					380					
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys	
385					390					395					400	
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg	
				405					410					415		
Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	
			420					425					430			
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	
		435					440					445				

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Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu
 450 455 460

Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
 465 470 475 480

Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
 485 490 495

Leu Ser Val Gln Glu Asp Val Lys Ile
 500 505

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCGAGGCGA GGTTTGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG 60

CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG 109
 Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg
 1 5 10

CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG GCG CTG 157
 Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu
 15 20 25

CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA 205
 Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys
 30 35 40

GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA 253
 Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr
 45 50 55

GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT 301
 Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile
 60 65 70 75

GAC	TTA	ATT	CCT	CGA	GAT	AGG	CCG	TTT	GTA	TGT	GCA	CCC	TCT	TCA	AAA	349
Asp	Leu	Ile	Pro	Arg	Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	
				80					85					90		
ACT	GGG	TCT	GTG	ACT	ACA	ACA	TAT	TGC	TGC	AAT	CAG	GAC	CAT	TGC	AAT	397
Thr	Gly	Ser	Val	Thr	Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	
			95					100					105			
AAA	ATA	GAA	CTT	CCA	ACT	ACT	GTA	AAG	TCA	TCA	CCT	GGC	CTT	GGT	CCT	445
Lys	Ile	Glu	Leu	Pro	Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	
		110					115					120				
GTG	GAA	CTG	GCA	GCT	GTC	ATT	GCT	GGA	CCA	GTG	TGC	TTC	GTC	TGC	ATC	493
Val	Glu	Leu	Ala	Ala	Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	
	125					130					135					
TCA	CTC	ATG	TTG	ATG	GTC	TAT	ATC	TGC	CAC	AAC	CGC	ACT	GTC	ATT	CAC	541
Ser	Leu	Met	Leu	Met	Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	
140					145					150					155	
CAT	CGA	GTG	CCA	AAT	GAA	GAG	GAC	CCT	TCA	TTA	GAT	CGC	CCT	TTT	ATT	589
His	Arg	Val	Pro	Asn	Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	
				160					165					170		
TCA	GAG	GGT	ACT	ACG	TTG	AAA	GAC	TTA	ATT	TAT	GAT	ATG	ACA	ACG	TCA	637
Ser	Glu	Gly	Thr	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	
			175					180					185			
GGT	TCT	GGC	TCA	GGT	TTA	CCA	TTG	CTT	GTT	CAG	AGA	ACA	ATT	GCG	AGA	685
Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	
		190					195					200				
ACT	ATT	GTG	TTA	CAA	GAA	AGC	ATT	GGC	AAA	GGT	CGA	TTT	GGA	GAA	GTT	733
Thr	Ile	Val	Leu	Gln	Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	
	205					210					215					
TGG	AGA	GGA	AAG	TGG	CGG	GGA	GAA	GAA	GTT	GCT	GTT	AAG	ATA	TTC	TCC	781
Trp	Arg	Gly	Lys	Trp	Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	
220					225					230					235	
TCT	AGA	GAA	GAA	CGT	TCG	TGG	TTC	CGT	GAG	GCA	GAG	ATT	TAT	CAA	ACT	829
Ser	Arg	Glu	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	
				240					245					250		
GTA	ATG	TTA	CGT	CAT	GAA	AAC	ATC	CTG	GGA	TTT	ATA	GCA	GCA	GAC	AAT	877
Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	
			255					260					265			
AAA	GAC	AAT	GGT	ACT	TGG	ACT	CAG	CTC	TGG	TTG	GTG	TCA	GAT	TAT	CAT	925
Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	
		270					275					280				

GAG Glu 285	CAT His	GGA Gly	TCC Ser	CTT Leu	TTT Phe	GAT Asp 290	TAC Tyr	TTA Leu	AAC Asn	AGA Arg	TAC Tyr 295	ACA Thr	GTT Val	ACT Thr	GTG Val	973
GAA Glu 300	GGA Gly	ATG Met	ATA Ile	AAA Lys	CTT Leu 305	GCT Ala	CTG Leu	TCC Ser	ACG Thr	GCG Ala 310	AGC Ser	GGT Gly	CTT Leu	GCC Ala	CAT His 315	1021
CTT Leu	CAC His	ATG Met	GAG Glu	ATT Ile 320	GTT Val	GGT Gly	ACC Thr	CAA Gln	GGA Gly 325	AAG Lys	CCA Pro	GCC Ala	ATT Ile	GCT Ala 330	CAT His	1069
AGA Arg	GAT Asp	TTG Leu	AAA Lys 335	TCA Ser	AAG Lys	AAT Asn	ATC Ile	TTG Leu 340	GTA Val	AAG Lys	AAG Lys	AAT Asn	GGA Gly 345	ACT Thr	TGC Cys	1117
TGT Cys	ATT Ile	GCA Ala 350	GAC Asp	TTA Leu	GGA Gly	CTG Leu	GCA Ala 355	GTA Val	AGA Arg	CAT His	GAT Asp	TCA Ser 360	GCC Ala	ACA Thr	GAT Asp	1165
ACC Thr 365	ATT Ile	GAT Asp	ATT Ile	GCT Ala	CCA Pro	AAC Asn 370	CAC His	AGA Arg	GTG Val	GGA Gly 375	ACA Thr	AAA Lys	AGG Arg	TAC Tyr	ATG Met	1213
GCC Ala 380	CCT Pro	GAA Glu	GTT Val	CTC Leu	GAT Asp 385	GAT Asp	TCC Ser	ATA Ile	AAT Asn	ATG Met 390	AAA Lys	CAT His	TTT Phe	GAA Glu	TCC Ser 395	1261
TTC Phe	AAA Lys	CGT Arg	GCT Ala	GAC Asp 400	ATC Ile	TAT Tyr	GCA Ala	ATG Met	GGC Gly 405	TTA Leu	GTA Val	TTC Phe	TGG Trp	GAA Glu 410	ATT Ile	1309
GCT Ala	CGA Arg	CGA Arg	TGT Cys 415	TCC Ser	ATT Ile	GGT Gly	GGA Gly	ATT Ile 420	CAT His	GAA Glu	GAT Asp	TAC Tyr 425	CAA Gln	CTG Leu	CCT Pro	1357
TAT Tyr	TAT Tyr	GAT Asp 430	CTT Leu	GTA Val	CCT Pro	TCT Ser	GAC Asp 435	CCA Pro	TCA Ser	GTT Val	GAA Glu	GAA Glu 440	ATG Met	AGA Arg	AAA Lys	1405
GTT Val 445	GTT Val	TGT Cys	GAA Glu	CAG Gln	AAG Lys	TTA Leu 450	AGG Arg	CCA Pro	AAT Asn	ATC Ile 455	CCA Pro	AAC Asn	AGA Arg	TGG Trp	CAG Gln	1453
AGC Ser 460	TGT Cys	GAA Glu	GCC Ala	TTG Leu	AGA Arg 465	GTA Val	ATG Met	GCT Ala	AAA Lys	ATT Ile 470	ATG Met	AGA Arg	GAA Glu	TGT Cys	TGG Trp 475	1501
TAT Tyr	GCC Ala	AAT Asn	GGA Gly	GCA Ala	GCT Ala 480	AGG Arg	CTT Leu	ACA Thr	GCA Ala 485	TTG Leu	CGG Arg	ATT Ile	AAG Lys	AAA Lys 490	ACA Thr	1549

TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA 1595
 Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met
 495 500

GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT TTGGGAGGTC 1655
 AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTTGC AGCAGTGTA 1715
 TAAAGTCAAT TAAAACTTC CCAGGATTTC TTTGGACCCA GGAAACAGCC ATGTGGGTCC 1775
 TTTCTGTGCA CTATGAACGC TTCTTTCCCA GGACAGAAAA TGTGTAGTCT ACCTTTATTT 1835
 TTTATTAACA AACTTGTTT TTTAAAAAGA TGATTGCTGG TCTTAACTTT AGGTA ACTCT 1895
 GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA CAATGAAACA 1955
 TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA 2015
 CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTACTGTT CTATAGTTTT TCAGGATCTT 2075
 AAAACTAACA CTTATAAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA TAGTAGTGAG 2135
 GAACATAATT CATGCAATTG TATTTTGTAT ACTATTATTG TTCTTTCCT TATTCAGAAC 2195
 ATTACATGCC TTCAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTTCT 2255
 AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT 2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg Leu Leu Leu Leu Val
 1 5 10 15

Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly Ala Thr
 20 25 30

Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
 35 40 45

Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys
 50 55 60

Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
 65 70 75 80

Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	Thr	Gly	Ser	Val	Thr	85	90	95
Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	Lys	Ile	Glu	Leu	Pro	100	105	110
Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	Val	Glu	Leu	Ala	Ala	115	120	125
Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	Ser	Leu	Met	Leu	Met	130	135	140
Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	His	Arg	Val	Pro	Asn	145	150	155
Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	Ser	Glu	Gly	Thr	Thr	165	170	175
Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	Gly	Ser	Gly	Ser	Gly	180	185	190
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	Thr	Ile	Val	Leu	Gln	195	200	205
Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	Lys	Trp	210	215	220
Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	Glu	Arg	225	230	235
Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	Arg	His	245	250	255
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	Gly	Thr	260	265	270
Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	Ser	Leu	275	280	285
Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	Glu	Gly	Met	Ile	Lys	290	295	300
Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	Glu	Ile	305	310	315
Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	325	330	335
Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	340	345	350
Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	Thr	Ile	Asp	Ile	Ala	355	360	365

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
 370 375 380

Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
 385 390 395 400

Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
 405 410 415

Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
 420 425 430

Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
 435 440 445

Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
 450 455 460

Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
 465 470 475 480

Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
 485 490 495

Gln Gln Glu Gly Ile Lys Met
 500

B' (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT 60

TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC 120

GGGGGTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC CTGTTGCCGG 180

CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC 240

ATG	ACC	TTG	GGG	AGC	TTC	AGA	AGG	GGC	CTT	TTG	ATG	CTG	TCG	GTG	GCC	288
Met	Thr	Leu	Gly	Ser	Phe	Arg	Arg	Gly	Leu	Leu	Met	Leu	Ser	Val	Ala	
1				5					10					15		
TTG	GGC	CTA	ACC	CAG	GGG	AGA	CTT	GCG	AAG	CCT	TCC	AAG	CTG	GTG	AAC	336
Leu	Gly	Leu	Thr	Gln	Gly	Arg	Leu	Ala	Lys	Pro	Ser	Lys	Leu	Val	Asn	
			20					25					30			
TGC	ACT	TGT	GAG	AGC	CCA	CAC	TGC	AAG	AGA	CCA	TTC	TGC	CAG	GGG	TCA	384
Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Arg	Pro	Phe	Cys	Gln	Gly	Ser	
		35					40					45				
TGG	TGC	ACA	GTG	GTG	CTG	GTT	CGA	GAG	CAG	GGC	AGG	CAC	CCC	CAG	GTC	432
Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Gln	Gly	Arg	His	Pro	Gln	Val	
	50					55					60					
TAT	CGG	GGC	TGT	GGG	AGC	CTG	AAC	CAG	GAG	CTC	TGC	TTG	GGA	CGT	CCC	480
Tyr	Arg	Gly	Cys	Gly	Ser	Leu	Asn	Gln	Glu	Leu	Cys	Leu	Gly	Arg	Pro	
65					70					75					80	
ACG	GAG	TTT	CTG	AAC	CAT	CAC	TGC	TGC	TAT	AGA	TCC	TTC	TGC	AAC	CAC	528
Thr	Glu	Phe	Leu	Asn	His	His	Cys	Cys	Tyr	Arg	Ser	Phe	Cys	Asn	His	
				85					90					95		
AAC	GTG	TCT	CTG	ATG	CTG	GAG	GCC	ACC	CAA	ACT	CCT	TCG	GAG	GAG	CCA	576
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro	
			100					105					110			
B' cont. GAA	GTT	GAT	GCC	CAT	CTG	CCT	CTG	ATC	CTG	GGT	CCT	GTG	CTG	GCC	TTG	624
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	
		115					120					125				
CCG	GTC	CTG	GTG	GCC	CTG	GGT	GCT	CTG	GGC	TTG	TGG	CGT	GTC	CGG	CGG	672
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg	
	130					135					140					
AGG	CAG	GAG	AAG	CAG	CGG	GAT	TTG	CAC	AGT	GAC	CTG	GGC	GAG	TCC	AGT	720
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser	
145					150					155					160	
CTC	ATC	CTG	AAG	GCA	TCT	GAA	CAG	GCA	GAC	AGC	ATG	TTG	GGG	GAC	TTC	768
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe	
				165					170					175		
CTG	GAC	AGC	GAC	TGT	ACC	ACG	GGC	AGC	GGC	TCG	GGG	CTC	CCC	TTC	TTG	816
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	
			180					185					190			
GTG	CAG	AGG	ACG	GTA	GCT	CGG	CAG	GTT	GCG	CTG	GTA	GAG	TGT	GTG	GGA	864
Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	
		195					200					205				

65

AAG Lys 210	GGC Gly 210	CGA Arg 210	TAT Tyr 210	GGC Gly 210	GAG Glu 215	GTG Val 215	TGG Trp 215	CGC Arg 215	GGT Gly 215	TCG Ser 220	TGG Trp 220	CAT His 220	GGC Gly 220	GAA Glu 220	AGC Ser 220	912
GTG Val 225	GCG Ala 225	GTC Val 225	AAG Lys 225	ATT Ile 230	TTC Phe 230	TCC Ser 230	TCA Ser 230	CGA Arg 230	GAT Asp 235	GAG Glu 235	CAG Gln 235	TCC Ser 235	TGG Trp 235	TTC Phe 240	CGG Arg 240	960
GAG Glu 245	ACG Thr 245	GAG Glu 245	ATC Ile 245	TAC Tyr 245	AAC Asn 245	ACA Thr 245	GTT Val 250	CTG Leu 250	CTT Leu 250	AGA Arg 250	CAC His 250	GAC Asp 255	AAC Asn 255	ATC Ile 255	CTA Leu 255	1008
GGC Gly 260	TTC Phe 260	ATC Ile 260	GCC Ala 260	TCC Ser 260	GAC Asp 265	ATG Met 265	ACT Thr 265	TCG Ser 265	CGG Arg 265	AAC Asn 270	TCG Ser 270	AGC Ser 270	ACG Thr 270	CAG Gln 270	CTG Leu 270	1056
TGG Trp 275	CTC Leu 275	ATC Ile 275	ACC Thr 275	CAC His 280	TAC Tyr 280	CAT His 280	GAA Glu 280	CAC His 280	GGC Gly 285	TCC Ser 285	CTC Leu 285	TAT Tyr 285	GAC Asp 285	TTT Phe 285	CTG Leu 285	1104
CAG Gln 290	AGG Arg 290	CAG Gln 290	ACG Thr 290	CTG Leu 295	GAG Glu 295	CCC Pro 295	CAG Gln 295	TTG Leu 295	GCC Ala 300	CTG Leu 300	AGG Arg 300	CTA Leu 300	GCT Ala 300	GTG Val 300	TCC Ser 300	1152
CCG Pro 305	GCC Ala 305	TGC Cys 310	GGC Gly 310	CTG Leu 310	GCG Ala 310	CAC His 310	CTA Leu 310	CAT His 315	GTG Val 315	GAG Glu 315	ATC Ile 315	TTT Phe 320	GGC Gly 320	ACT Thr 320	CAA Gln 320	1200
GGC Gly 325	AAA Lys 325	CCA Pro 325	GCC Ala 325	ATT Ile 325	GCC Ala 330	CAT His 330	CGT Arg 330	GAC Asp 330	CTC Leu 330	AAG Lys 335	AGT Ser 335	CGC Arg 335	AAT Asn 335	GTG Val 335	CTG Leu 335	1248
GTC Val 340	AAG Lys 340	AGT Ser 340	AAC Asn 340	TTG Leu 340	CAG Gln 345	TGT Cys 345	TGC Cys 345	ATT Ile 345	GCA Ala 350	GAC Asp 350	CTG Leu 350	GGA Gly 350	CTG Leu 350	GCT Ala 350	GTG Val 350	1296
ATG Met 355	CAC His 355	TCA Ser 355	CAA Gln 355	AGC Ser 360	AAC Asn 360	GAG Glu 360	TAC Tyr 360	CTG Leu 360	GAT Asp 365	ATC Ile 365	GGC Gly 365	AAC Asn 365	ACA Thr 365	CCC Pro 365	CGA Arg 365	1344
GTG Val 370	GGT Gly 370	ACC Thr 370	AAA Lys 375	AGA Arg 375	TAC Tyr 375	ATG Met 375	GCA Ala 380	CCC Pro 380	GAG Glu 380	GTG Val 380	CTG Leu 380	GAT Asp 380	GAG Glu 380	CAC His 380	ATC Ile 380	1392
CGC Arg 385	ACA Thr 385	GAC Asp 390	TGC Cys 390	TTT Phe 390	GAG Glu 390	TCG Ser 395	TAC Tyr 395	AAG Lys 395	TGG Trp 395	ACA Thr 395	GAC Asp 395	ATC Ile 400	TGG Trp 400	GCC Ala 400	TTT Phe 400	1440
GGC Gly 405	CTA Leu 405	GTG Val 405	CTA Leu 405	TGG Trp 405	GAG Glu 410	ATC Ile 410	GCC Ala 410	CGG Arg 410	CGG Arg 410	ACC Thr 415	ATC Ile 415	ATC Ile 415	AAT Asn 415	GGC Gly 415	ATT Ile 415	1488

67

66

GTG	GAG	GAT	TAC	AGG	CCA	CCT	TTC	TAT	GAC	ATG	GTA	CCC	AAT	GAC	CCC	1536
Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Met	Val	Pro	Asn	Asp	Pro	
			420					425					430			
AGT	TTT	GAG	GAC	ATG	AAA	AAG	GTG	GTG	TGC	GTT	GAC	CAG	CAG	ACA	CCC	1584
Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	Pro	
		435					440					445				
ACC	ATC	CCT	AAC	CGG	CTG	GCT	GCA	GAT	CCG	GTC	CTC	TCC	GGG	CTG	GCC	1632
Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu	Ala	
		450				455					460					
CAG	ATG	ATG	AGA	GAG	TGC	TGG	TAC	CCC	AAC	CCC	TCT	GCT	CGC	CTC	ACC	1680
Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu	Thr	
465					470					475					480	
GCA	CTG	CGC	ATA	AAG	AAG	ACA	TTG	CAG	AAG	CTC	AGT	CAC	AAT	CCA	GAG	1728
Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Leu	Ser	His	Asn	Pro	Glu	
				485					490					495		
AAG	CCC	AAA	GTG	ATT	CAC	TAGCCCAGGG	CCACCAGGCT	TCCTCTGCCT								1776
Lys	Pro	Lys	Val	Ile	His											
			500													
AAAGTGTGTG	CTGGGGAAGA	AGACATAGCC	TGTCTGGGTA	GAGGGAGTGA	AGAGAGTGTG											1836
CACGCTGCCC	TGTGTGTGCC	TGCTCAGCTT	GCTCCCAGCC	CATCCAGCCA	AAAATACAGC											1896
TGAGCTGAAA	TTCAAAAAAA	AAAAAA														1922

B' ant.

- (2) INFORMATION FOR SEQ ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Thr	Leu	Gly	Ser	Phe	Arg	Arg	Gly	Leu	Leu	Met	Leu	Ser	Val	Ala	
1				5					10					15		
Leu	Gly	Leu	Thr	Gln	Gly	Arg	Leu	Ala	Lys	Pro	Ser	Lys	Leu	Val	Asn	
			20					25					30			
Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Arg	Pro	Phe	Cys	Gln	Gly	Ser	
		35					40					45				
Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Gln	Gly	Arg	His	Pro	Gln	Val	
		50				55					60					

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Tyr	Arg	Gly	Cys	Gly	Ser	Leu	Asn	Gln	Glu	Leu	Cys	Leu	Gly	Arg	Pro
65					70					75					80
Thr	Glu	Phe	Leu	Asn	His	His	Cys	Cys	Tyr	Arg	Ser	Phe	Cys	Asn	His
				85					90					95	
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro
			100					105					110		
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu
		115					120					125			
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg
	130					135					140				
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser
145					150					155					160
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe
				165					170					175	
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu
			180					185					190		
Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly
		195					200					205			
Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser
	210					215					220				
Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg
225					230					235					240
Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu
				245					250					255	
Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu
			260					265					270		
Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu
		275					280					285			
Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser
	290					295					300				
Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln
305					310					315					320
Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu
				325					330					335	
Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val
			340					345					350		

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Met-His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg
 355 360 365

Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile
 370 375 380

Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe
 385 390 395 400

Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile
 405 410 415

Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro
 420 425 430

Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro
 435 440 445

Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala
 450 455 460

Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr
 465 470 475 480

Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu
 485 490 495

Lys Pro Lys Val Ile His
 500

B' cont.
 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTCGGAGAA ATTGGAAC TA CAGTTTTATC	60
TAGCCACATC TCTGAGAATT CTGAAGAAAG CAGCAGGTGA AAGTCATTGC CAAGTGATTT	120
TGTTCTGTAA GGAAGCCTCC CTCATTCACT TACACCAGTG AGACAGCAGG ACCAGTCATT	180

CAAAGGGCCG	TGTACAGGAC	GCGTGGCAAT	CAGACA	ATG	ACT	CAG	CTA	TAC	ACT								234
				Met	Thr	Gln	Leu	Tyr	Thr								
				1				5									
TAC	ATC	AGA	TTA	CTG	GGA	GCC	TGT	CTG	TTC	ATC	ATT	TCT	CAT	GTT	CAA		282
Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe	Ile	Ile	Ser	His	Val	Gln		
			10					15						20			
GGG	CAG	AAT	CTA	GAT	AGT	ATG	CTC	CAT	GGC	ACT	GGT	ATG	AAA	TCA	GAC		330
Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly	Thr	Gly	Met	Lys	Ser	Asp		
		25					30					35					
TTG	GAC	CAG	AAG	AAG	CCA	GAA	AAT	GGA	GTG	ACT	TTA	GCA	CCA	GAG	GAT		378
Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val	Thr	Leu	Ala	Pro	Glu	Asp		
	40					45					50						
ACC	TTG	CCT	TTC	TTA	AAG	TGC	TAT	TGC	TCA	GGA	CAC	TGC	CCA	GAT	GAT		426
Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	Gly	His	Cys	Pro	Asp	Asp		
	55				60					65					70		
GCT	ATT	AAT	AAC	ACA	TGC	ATA	ACT	AAT	GGC	CAT	TGC	TTT	GCC	ATT	ATA		474
Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	His	Cys	Phe	Ala	Ile	Ile		
				75					80					85			
GAA	GAA	GAT	GAT	CAG	GGA	GAA	ACC	ACA	TTA	ACT	TCT	GGG	TGT	ATG	AAG		522
Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	Thr	Ser	Gly	Cys	Met	Lys		
			90					95					100				
TAT	GAA	GGC	TCT	GAT	TTT	CAA	TGC	AAG	GAT	TCA	CCG	AAA	GCC	CAG	CTA		570
Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	Ser	Pro	Lys	Ala	Gln	Leu		
		105					110					115					
CGC	AGG	ACA	ATA	GAA	TGT	TGT	CGG	ACC	AAT	TTG	TGC	AAC	CAG	TAT	TTG		618
Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	Leu	Cys	Asn	Gln	Tyr	Leu		
	120					125					130						
CAG	CCT	ACA	CTG	CCC	CCT	GTT	GTT	ATA	GGT	CCG	TTC	TTT	GAT	GGC	AGC		666
Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser		
	135				140					145					150		
ATC	CGA	TGG	CTG	GTT	GTG	CTC	ATT	TCC	ATG	GCT	GTC	TGT	ATA	GTT	GCT		714
Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met	Ala	Val	Cys	Ile	Val	Ala		
				155					160					165			
ATG	ATC	ATC	TTC	TCC	AGC	TGC	TTT	TGC	TAT	AAG	CAT	TAT	TGT	AAG	AGT		762
Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser		
			170					175					180				
ATC	TCA	AGC	AGG	GGT	CGT	TAC	AAC	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA		810
Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala		
			185				190					195					

TTT	ATT	CCA	GTA	GGA	GAA	TCA	TTG	AAA	GAC	CTG	ATT	GAC	CAG	TCC	CAA	858
Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	
200						205					210					
AGC	TCT	GGG	AGT	GGA	TCT	GGA	TTG	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	906
Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	
215					220					225					230	
GCC	AAA	CAG	ATT	CAG	ATG	GTT	CGG	CAG	GTT	GGT	AAA	GGC	CGC	TAT	GGA	954
Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	
				235					240					245		
GAA	GTA	TGG	ATG	GGT	AAA	TGG	CGT	GGT	GAA	AAA	GTG	GCT	GTC	AAA	GTG	1002
Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	
			250					255					260			
TTT	TTT	ACC	ACT	GAA	GAA	GCT	AGC	TGG	TTT	AGA	GAA	ACA	GAA	ATC	TAC	1050
Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	
		265					270					275				
CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	CTT	GGT	TTT	ATA	GCT	GCA	1098
Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	
		280				285					290					
GAC	ATT	AAA	GGC	ACT	GGT	TCC	TGG	ACT	CAG	CTG	TAT	TTG	ATT	ACT	GAT	1146
Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	
295					300					305					310	
TAC	CAT	GAA	AAT	GGA	TCT	CTC	TAT	GAC	TTC	CTG	AAA	TGT	GCC	ACA	CTA	1194
Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu	
				315					320					325		
GAC	ACC	AGA	GCC	CTA	CTC	AAG	TTA	GCT	TAT	TCT	GCT	GCT	TGT	GGT	CTG	1242
Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu	
			330					335					340			
TGC	CAC	CTC	CAC	ACA	GAA	ATT	TAT	GGT	ACC	CAA	GGG	AAG	CCT	GCA	ATT	1290
Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	
			345				350					355				
GCT	CAT	CGA	GAC	CTG	AAG	AGC	AAA	AAC	ATC	CTT	ATT	AAG	AAA	AAT	GGA	1338
Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly	
		360				365				370						
AGT	TGC	TGT	ATT	GCT	GAC	CTG	GGC	CTA	GCT	GTT	AAA	TTC	AAC	AGT	GAT	1386
Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp	
375					380					385					390	
ACA	AAT	GAA	GTT	GAC	ATA	CCC	TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAG	CGG	1434
Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	
				395					400					405		

TAC	ATG	GCT	CCA	GAA	GTG	CTG	GAT	GAA	AGC	CTG	AAT	AAA	AAC	CAT	TTC	1482
Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe	
			410					415					420			
CAG	CCC	TAC	ATC	ATG	GCT	GAC	ATC	TAT	AGC	TTT	GGT	TTG	ATC	ATT	TGG	1530
Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp	
		425					430					435				
GAA	ATG	GCT	CGT	CGT	TGT	ATT	ACA	GGA	GGA	ATC	GTG	GAG	GAA	TAT	CAA	1578
Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	
	440					445					450					
TTA	CCA	TAT	TAC	AAC	ATG	GTG	CCC	AGT	GAC	CCA	TCC	TAT	GAG	GAC	ATG	1626
Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	
455					460					465					470	
CGT	GAG	GTT	GTG	TGT	GTG	AAA	CGC	TTG	CGG	CCA	ATC	GTG	TCT	AAC	CGC	1674
Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	
				475				480						485		
TGG	AAC	AGC	GAT	GAA	TGT	CTT	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	1722
Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	
			490					495					500			
TGT	TGG	GCC	CAT	AAT	CCA	GCC	TCC	AGA	CTC	ACA	GCT	TTG	AGA	ATC	AAG	1770
Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	
		505					510					515				
AAG	ACA	CTT	GCA	AAA	ATG	GTT	GAA	TCC	CAG	GAT	GTA	AAG	ATT			1812
Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln	Asp	Val	Lys	Ile			
		520				525					530					
TGACAATTAA	ACAATTTTGA	GGGAGAATTT	AGACTGCAAG	AACTTCTTCA	CCCAAGGAAT											1872
GGGTGGGATT	AGCATGGAAT	AGGATGTTGA	CTTGGTTTCC	AGACTCCTTC	CTCTACATCT											1932
TCACAGGCTG	CTAACAGTAA	ACCTTACCGT	ACTCTACAGA	ATACAAGATT	GGAAGTTGGA											1992
ACTTCAAACA	TGTCATTTCTT	TATATATGAC	AGCTTTGTTT	TAATGTGGGG	TTTTTTTGT											2052
TGCTTTTTTTT	GTTTTGTT															2070

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe
 1 5 10 15

Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
 20 25 30
 Thr Gly Met Lys Ser Asp Leu Asp Gln Lys Lys Pro Glu Asn Gly Val
 35 40 45
 Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
 50 55 60
 Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
 65 70 75 80
 His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
 85 90 95
 Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
 100 105 110
 Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
 115 120 125
 Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
 130 135 140
 Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Val Leu Ile Ser Met
 145 150 155 160
 Ala Val Cys Ile Val Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
 165 170 175
 Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp
 180 185 190
 Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
 195 200 205
 Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
 210 215 220
 Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
 225 230 235 240
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
 245 250 255
 Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
 260 265 270
 Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
 275 280 285
 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
 290 295 300

Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
 305 310 315 320
 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
 325 330 335
 Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
 340 345 350
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
 355 360 365
 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
 370 375 380
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr
 385 390 395 400
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
 485 490 495
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
 500 505 510
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
 515 520 525
 Asp Val Lys Ile
 530

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu	
1 5 10	
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC	96
Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile	
15 20 25	
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC	144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr	
30 35 40 45	
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	
AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG	384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val	
110 115 120 125	
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC	432
Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile	
130 135 140	

ATT Ile	ATC Ile	ATC Ile	GTC Val 145	TTC Phe	CTG Leu	GTC Val	ATC Ile	AAC Asn 150	TAT Tyr	CAC His	CAG Gln	CGT Arg	GTC Val 155	TAC Tyr	CAT His	480
AAC Asn	CGC Arg	CAG Gln 160	AGG Arg	TTG Leu	GAC Asp	ATG Met	GAG Glu 165	GAC Asp	CCC Pro	TCT Ser	TGC Cys	GAG Glu 170	ATG Met	TGT Cys	CTC Leu	528
TCC Ser	AAA Lys 175	GAC Asp	AAG Lys	ACG Thr	CTC Leu	CAG Gln 180	GAT Asp	CTC Leu	GTC Val	TAC Tyr	GAC Asp 185	CTC Leu	TCC Ser	ACG Thr	TCA Ser	576
GGG Gly 190	TCT Ser	GGC Gly	TCA Ser	GGG Gly	TTA Leu 195	CCC Pro	CTT Leu	TTT Phe	GTC Val	CAG Gln 200	CGC Arg	ACA Thr	GTG Val	GCC Ala	CGA Arg 205	624
ACC Thr	ATT Ile	GTT Val	TTA Leu	CAA Gln 210	GAG Glu	ATT Ile	ATC Ile	GGC Gly 215	AAG Lys	GGC Gly	CGG Arg	TTC Phe	GGG Gly 220	GAA Glu	GTA Val	672
TGG Trp	CGT Arg	GGT Gly 225	CGC Arg	TGG Trp	AGG Arg	GGT Gly	GGT Gly	GAC Asp 230	GTG Val	GCT Ala	GTG Val	AAA Lys	ATC Ile 235	TTC Phe	TCT Ser	720
TCT Ser	CGT Arg	GAA Glu 240	GAA Glu	CGG Arg	TCT Ser	TGG Trp	TTC Phe 245	CGT Arg	GAA Glu	GCA Ala	GAG Glu	ATC Ile 250	TAC Tyr	CAG Gln	ACC Thr	768
<i>B' cont.</i> GTC Val 255	ATG Met	CTG Leu	CGC Arg	CAT His	GAA Glu	AAC Asn 260	ATC Ile	CTT Leu	GGC Gly	TTT Phe	ATT Ile 265	GCT Ala	GCT Ala	GAC Asp	AAT Asn	816
AAA Lys 270	GAT Asp	AAT Asn	GGC Gly	ACC Thr	TGG Trp 275	ACC Thr	CAG Gln	CTG Leu	TGG Trp	CTT Leu 280	GTC Val	TCT Ser	GAC Asp	TAT Tyr	CAC His 285	864
GAG Glu	CAT His	GGC Gly	TCA Ser	CTG Leu	TTT Phe	GAT Asp	TAT Tyr	CTG Leu	AAC Asn 295	CGC Arg	TAC Tyr	ACA Thr	GTG Val	ACC Thr 300	ATT Ile	912
GAG Glu	GGA Gly	ATG Met	ATT Ile	AAG Lys	CTA Leu	GCC Ala	TTG Leu	TCT Ser	GCA Ala	GCC Ala	AGT Ser	GGT Gly	TTG Leu 315	GCA Ala	CAC His	960
CTG Leu	CAT His	ATG Met	GAG Glu	ATT Ile	GTG Val	GGC Gly	ACT Thr	CAA Gln	GGG Gly	AAG Lys	CCG Pro	GGA Gly 330	ATT Ile	GCT Ala	CAT His	1008
CGA Arg	GAC Asp 335	TTG Leu	AAG Lys	TCA Ser	AAG Lys	AAC Asn 340	ATC Ile	CTG Leu	GTG Val	AAA Lys	AAA Lys	AAT Asn 345	GGC Gly	ATG Met	TGT Cys	1056

GCC	ATT	GCA	GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCG	GTC	ACT	GAC	1104
Ala	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	
350					355					360					365	
ACC	ATA	GAC	ATT	GCT	CCA	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	1152
Thr	Ile	Asp	Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	
				370					375						380	
GCT	CCT	GAA	GTC	CTT	GAC	GAG	ACA	ATC	AAC	ATG	AAG	CAC	TTT	GAC	TCC	1200
Ala	Pro	Glu	Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	
			385					390						395		
TTC	AAA	TGT	GCC	GAC	ATC	TAT	GCC	CTC	GGG	CTT	GTC	TAC	TGG	GAG	ATT	1248
Phe	Lys	Cys	Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	
		400					405					410				
GCA	CGA	AGA	TGC	AAT	TCT	GGA	GGA	GTC	CAT	GAA	GAC	TAT	CAA	CTG	CCG	1296
Ala	Arg	Arg	Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Asp	Tyr	Gln	Leu	Pro	
	415					420					425					
TAT	TAC	GAC	TTA	GTG	CCC	TCC	GAC	CCT	TCC	ATT	GAG	GAG	ATG	CGA	AAG	1344
Tyr	Tyr	Asp	Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	
430					435					440					445	
GTT	GTA	TGT	GAC	CAG	AAG	CTA	CGG	CCC	AAT	GTC	CCC	AAC	TGG	TGG	CAG	1392
Val	Val	Cys	Asp	Gln	Lys	Leu	Arg	Pro	Asn	Val	Pro	Asn	Trp	Trp	Gln	
				450					455					460		
AGT	TAT	GAG	GCC	TTG	CGA	GTG	ATG	GGA	AAG	ATG	ATG	CGG	GAG	TGC	TGG	1440
Ser	Tyr	Glu	Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	
			465					470					475			
TAC	GCC	AAT	GGT	GCT	GCC	CGT	CTG	ACA	GCT	CTG	CGC	ATC	AAG	AAG	ACT	1488
Tyr	Ala	Asn	Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	
		480					485					490				
CTG	TCC	CAG	CTA	AGC	GTG	CAG	GAA	GAT	GTG	AAG	ATT	TAAGCTGTTC				1534
Leu	Ser	Gln	Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile					
	495					500					505					
CTCTGCCTAC	ACAAAGAACC	TGGGCAGTGA	GGATGACTGC	AGCCACCGTG	CAAGCGTCGT											1594
GGAGGCCTAT	CCTCTTGTTT	CTGCCCCGCC	CTCTGGCAGA	GCCCTGGCCT	GCAAGAGGGA											1654
CAGAGCCTGG	GAGACGCGCG	CACTCCCGTT	GGGTTTGAGA	CAGACACTTT	TTATATTTAC											1714
CTCCTGATGG	CATGGAGACC	TGAGCAAATC	ATGTAGTCAC	TCAATGCCAC	AACTCAAAC											1774
GCTTCAGTGG	GAAGTACAGA	GACCCAGTGC	ATTGCGTGTG	CAGGAGCGTG	AGGTGCTGGG											1834
CTCGCCAGGA	GCGGCCCCCA	TACCTTGTGG	TCCACTGGGC	TGCAGGTTTT	CCTCCAGGGA											1894
CCAGTCAACT	GGCATCAAGA	TATTGAGAGG	AACCGGAAGT	TTCTCCCTCC	TTCCCGTAGC											1954

AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCCTA GAGACACAAC 2014
 CTGCTGCCTG TCTGTCCAGC CAAGTGCGCA TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG 2074
 GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA 2134
 ACCTGCTTGA GCTTCTGTGC ATGTGT 2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
 1 5 10 15
 Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu
 20 25 30
 Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr
 35 40 45
 Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His
 50 55 60
 His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
 65 70 75 80
 Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
 85 90 95
 Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His
 100 105 110
 Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val
 115 120 125
 Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
 130 135 140
 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
 145 150 155 160
 Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
 165 170 175
 Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
 180 185 190

Ser-Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
 195 200 205
 Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
 210 215 220
 Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
 225 230 235 240
 Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
 245 250 255
 Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
 260 265 270
 Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
 275 280 285
 Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
 290 295 300
 Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
 305 310 315 320
 Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
 325 330 335
 Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
 340 345 350
 Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
 355 360 365
 Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
 370 375 380
 Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
 385 390 395 400
 Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
 405 410 415
 Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp
 420 425 430
 Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys
 435 440 445
 Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu
 450 455 460
 Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn
 465 470 475 480

Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln
 485 490 495

Leu Ser Val Gln Glu Asp Val Lys Ile
 500 505

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1952 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGCGGC AGAAGTTGCC GGC GTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC 60

TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC 120

AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT 180

b' mt. GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG 228
 Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys
 1 5 10

AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA 276
 Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu
 15 20 25 30

CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC 324
 Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile
 35 40 45

TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT 372
 Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser
 50 55 60

GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT 420
 Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp
 65 70 75

TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA 468
 Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu
 80 85 90

TGC Cys 95	TGC Cys	ACA Thr	GAA Glu	AGG Arg	AAT Asn 100	GAG Glu	TGT Cys	AAT Asn	AAA Lys	GAC Asp 105	CTC Leu	CAC His	CCC Pro	ACT Thr	CTG Leu 110	516
CCT Pro	CCT Pro	CTC Leu	AAG Lys	GAC Asp 115	AGA Arg	GAT Asp	TTT Phe	GTT Val	GAT Asp 120	GGG Gly	CCC Pro	ATA Ile	CAC His	CAC His 125	AAG Lys	564
GCC Ala	TTG Leu	CTT Leu	ATC Ile 130	TCT Ser	GTG Val	ACT Thr	GTC Val	TGT Cys 135	AGT Ser	TTA Leu	CTC Leu	TTG Leu	GTC Val 140	CTC Leu	ATT Ile	612
ATT Ile	TTA Leu	TTC Phe 145	TGT Cys	TAC Tyr	TTC Phe	AGG Arg	TAT Tyr 150	AAA Lys	AGA Arg	CAA Gln	GAA Glu	GCC Ala 155	CGA Arg	CCT Pro	CGG Arg	660
TAC Tyr 160	AGC Ser	ATT Ile	GGG Gly	CTG Leu	GAG Glu	CAG Gln 165	GAC Asp	GAG Glu	ACA Thr	TAC Tyr 170	ATT Ile	CCT Pro	CCT Pro	GGA Gly	GAG Glu	708
TCC Ser 175	CTG Leu	AGA Arg	GAC Asp	TTG Leu	ATC Ile 180	GAG Glu	CAG Gln	TCT Ser	CAG Gln	AGC Ser 185	TCG Ser	GGA Gly	AGT Ser	GGA Gly	TCA Ser 190	756
GGC Gly	CTC Leu	CCT Pro	CTG Leu	CTG Leu 195	GTC Val	CAA Gln	AGG Arg	ACA Thr	ATA Ile 200	GCT Ala	AAG Lys	CAA Gln	ATT Ile	CAG Gln 205	ATG Met	804
GTG Val	AAG Lys	CAG Gln	ATT Ile 210	GGA Gly	AAA Lys	GGC Gly	CGC Arg	TAT Tyr 215	GGC Gly	GAG Glu	GTG Val	TGG Trp	ATG Met 220	GGA Gly	AAG Lys	852
TGG Trp	CGT Arg	GGA Gly 225	GAA Glu	AAG Lys	GTG Val	GCT Ala	GTG Val 230	AAA Lys	GTG Val	TTC Phe	TTC Phe	ACC Thr 235	ACG Thr	GAG Glu	GAA Glu	900
GCC Ala 240	AGC Ser	TGG Trp	TTC Phe	CGA Arg	GAG Glu	ACT Thr 245	GAG Glu	ATA Ile	TAT Tyr	CAG Gln	ACG Thr	GTC Val	CTG Leu	ATG Met	CGG Arg	948
CAT His 255	GAG Glu	AAT Asn	ATT Ile	CTG Leu	GGG Gly 260	TTC Phe	ATT Ile	GCT Ala	GCA Ala	GAT Asp 265	ATC Ile	AAA Lys	GGG Gly	ACT Thr	GGG Gly 270	996
TCC Ser	TGG Trp	ACT Thr	CAG Gln	TTG Leu 275	TAC Tyr	CTC Leu	ATC Ile	ACA Thr	GAC Asp 280	TAT Tyr	CAT His	GAA Glu	AAC Asn	GGC Gly 285	TCC Ser	1044
CTT Leu	TAT Tyr	GAC Asp	TAT Tyr 290	CTG Leu	AAA Lys	TCC Ser	ACC Thr	ACC Thr 295	TTA Leu	GAC Asp	GCA Ala	AAG Lys	TCC Ser 300	ATG Met	CTG Leu	1092

AAG Lys	CTA Leu	GCC Ala 305	TAC Tyr	TCC Ser	TCT Ser	GTC Val	AGC Ser 310	GGC Gly	CTA Leu	TGC Cys	CAT His	TTA Leu 315	CAC His	ACG Thr	GAA Glu	1140		
ATC Ile	TTT Phe 320	AGC Ser	ACT Thr	CAA Gln	GGC Gly	AAG Lys 325	CCA Pro	GCA Ala	ATC Ile	GCC Ala	CAT His 330	CGA Arg	GAC Asp	TTG Leu	AAA Lys	1188		
AGT Ser 335	AAA Lys	AAC Asn	ATC Ile	CTG Leu	GTG Val 340	AAG Lys	AAA Lys	AAT Asn	GGA Gly	ACT Thr 345	TGC Cys	TGC Cys	ATA Ile	GCA Ala	GAC Asp 350	1236		
CTG Leu	GGC Gly	TTG Leu	GCT Ala	GTC Val 355	AAG Lys	TTC Phe	ATT Ile	AGT Ser	GAC Asp 360	ACA Thr	AAT Asn	GAG Glu	GTT Val	GAC Asp 365	ATC Ile	1284		
CCA Pro	CCC Pro	AAC Asn	ACC Thr 370	CGG Arg	GTT Val	GGC Gly	ACC Thr 375	AAG Lys	CGC Arg	TAT Tyr	ATG Met	CCT Pro	CCA Pro 380	GAA Glu	GTG Val	1332		
CTG Leu	GAC Asp	GAG Glu 385	AGC Ser	TTG Leu	AAT Asn	AGA Arg	AAC Asn 390	CAT His	TTC Phe	CAG Gln	TCC Ser	TAC Tyr 395	ATT Ile	ATG Met	GCT Ala	1380		
GAC Asp	ATG Met 400	TAC Tyr	AGC Ser	TTT Phe	GGA Gly	CTC Leu 405	ATC Ile	CTC Leu	TGG Trp	GAG Glu	ATT Ile 410	GCA Ala	AGG Arg	AGA Arg	TGT Cys	1428		
GTT Val 415	TCT Ser	GGA Gly	GGT Gly	ATA Ile	GTG Val 420	GAA Glu	GAA Glu	TAC Tyr	CAG Gln	CTT Leu 425	CCC Pro	TAT Tyr	CAC His	GAC Asp	CTG Leu 430	1476		
GTG Val	CCC Pro	AGT Ser	GAC Asp	CCT Pro 435	TCT Ser	TAT Tyr	GAG Glu	GAC Asp	ATG Met 440	AGA Arg	GAA Glu	ATT Ile	GTG Val	TGC Cys 445	ATG Met	1524		
AAG Lys	AAG Lys	TTA Leu	CGG Arg 450	CCT Pro	TCA Ser	TTC Phe	CCC Pro 455	AAT Asn	CGA Arg	TGG Trp	AGC Ser	AGT Ser	GAT Asp 460	GAG Glu	TGT Cys	1572		
CTC Leu	AGG Arg	CAG Gln 465	ATG Met	GGG Gly	AAG Lys	CTT Leu	ATG Met 470	ACA Thr	GAG Glu	TGC Cys	TGG Trp	GCG Ala 475	CAG Gln	AAT Asn	CCT Pro	1620		
GCC Ala	TCC Ser 480	AGG Arg	CTG Leu	ACG Thr	GCC Ala	CTG Leu 485	AGA Arg	GTT Val	AAG Lys	AAA Lys	ACC Thr 490	CTT Leu	GCC Ala	AAA Lys	ATG Met	1668		
TCA Ser 495	GAG Glu	TCC Ser	CAG Gln	GAC Asp	ATT Ile 500	AAA Lys	CTC Leu	TGACGTCAGA				TACTTGTGGA				CAGAGCAAGA		1722
ATTTACACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA																1782		

GACITTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT 1842
 CATGGCTTTC TGAGGAGGAG AAAC TGTGTTG GGTAAC TTGT TCAAGATATG ATGCATGTTG 1902
 CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTTT ATAAAAAAAAA 1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu
 1 5 10 15
 Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys
 20 25 30
 Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
 35 40 45
 Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met
 50 55 60
 Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
 65 70 75 80
 Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
 85 90 95
 Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
 100 105 110
 Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu
 115 120 125
 Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
 130 135 140
 Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser
 145 150 155 160
 Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
 165 170 175
 Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
 180 185 190
 Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195 200 205

83

Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	
210						215					220					
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	
225					230					235					240	
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	
				245					250					255		
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	
			260					265					270			
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	
		275					280					285				
Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	Lys	Leu	
	290					295					300					
Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Phe	
305					310					315					320	
Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	
				325					330					335		
Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	Gly	
			340					345					350			
Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Pro	
		355					360					365				
Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	Leu	Asp	
	370					375					380					
Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	Asp	Met	
385					390					395					400	
Tyr	Ser	Phe	Gly	Leu	Ile	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Val	Ser	
				405					410					415		
Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	His	Asp	Leu	Val	Pro	
			420					425					430			
Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Ile	Val	Cys	Met	Lys	Lys	
		435					440					445				
Leu	Arg	Pro	Ser	Phe	Pro	Asn	Arg	Trp	Ser	Ser	Asp	Glu	Cys	Leu	Arg	
	450					455					460					
Gln	Met	Gly	Lys	Leu	Met	Thr	Glu	Cys	Trp	Ala	Gln	Asn	Pro	Ala	Ser	
465					470					475					480	
Arg	Leu	Thr	Ala	Leu	Arg	Val	Lys	Lys	Thr	Leu	Ala	Lys	Met	Ser	Glu	
				485					490					495		

B' cont.

85

Ser Gln Asp Ile Lys Leu
500

- (2) INFORMATION FOR SEQ ID NO: 19:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

- B' cont.*
- (2) INFORMATION FOR SEQ ID NO: 20:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

- (2) INFORMATION FOR SEQ ID NO: 21:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

85

- (2) INFORMATION FOR SEQ ID NO: 22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CGGAATTCTG GTGCCATATA

20

- (2) INFORMATION FOR SEQ ID NO: 23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG

37

B' cont.

- (2) INFORMATION FOR SEQ ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCGGATCCAC CATGGCGGAG TCGGCC

26

87

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly Xaa Gly Xaa Xaa Gly
 1 5

B'
cont.

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn
 1 5

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn
 1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met

1

5

B'
conc.